

# Report

	assembly
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	3102796
Total length (>= 5000 bp)	3102796
Total length (>= 10000 bp)	3102796
Total length (>= 25000 bp)	3084669
Total length (>= 50000 bp)	2998930
# contigs	4
Largest contig	2998930
Total length	3102796
Reference length	2992342
GC (%)	38.08
Reference GC (%)	37.96
N50	2998930
NG50	2998930
N75	2998930
NG75	2998930
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	53716
Genome fraction (%)	99.964
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.71
# indels per 100 kbp	30.46
Largest alignment	2997381
Total aligned length	3048399
NA50	2997381
NGA50	2997381
NA75	2997381
NGA75	2997381
LA50	1
LGA50	1
LA75	1
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

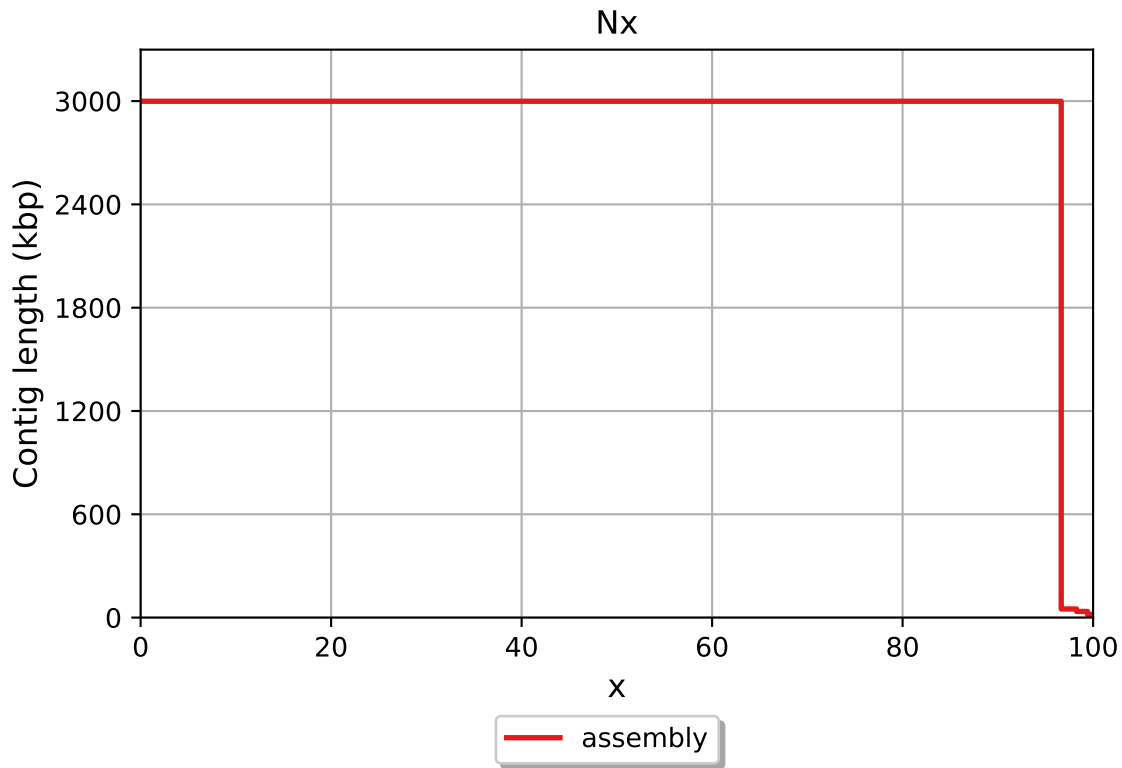
	assembly
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	2
# possible misassemblies	3
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	81
# indels	911
# indels (<= 5 bp)	910
# indels (> 5 bp)	1
Indels length	1029

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

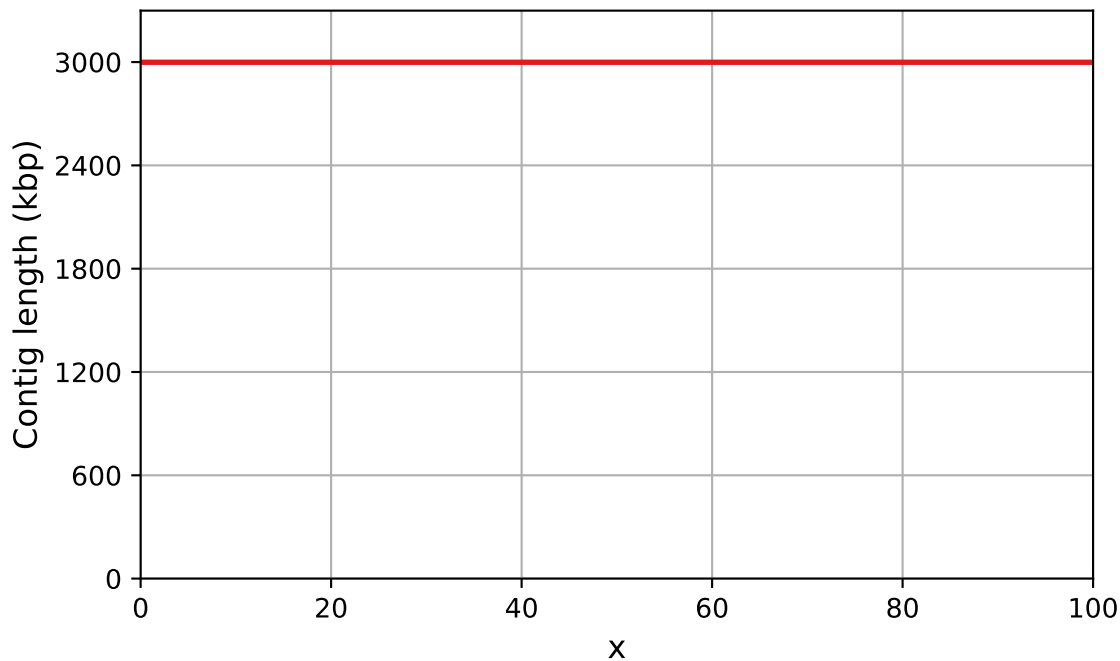
## Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	53716
# N's	0

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

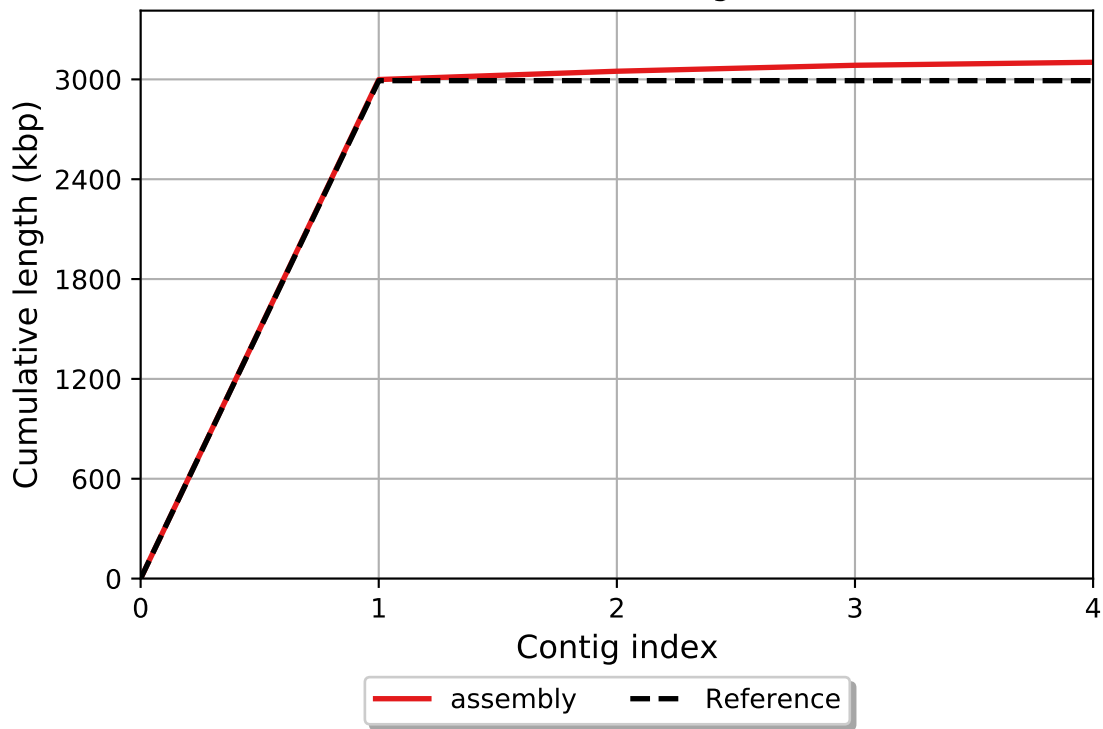


NGx

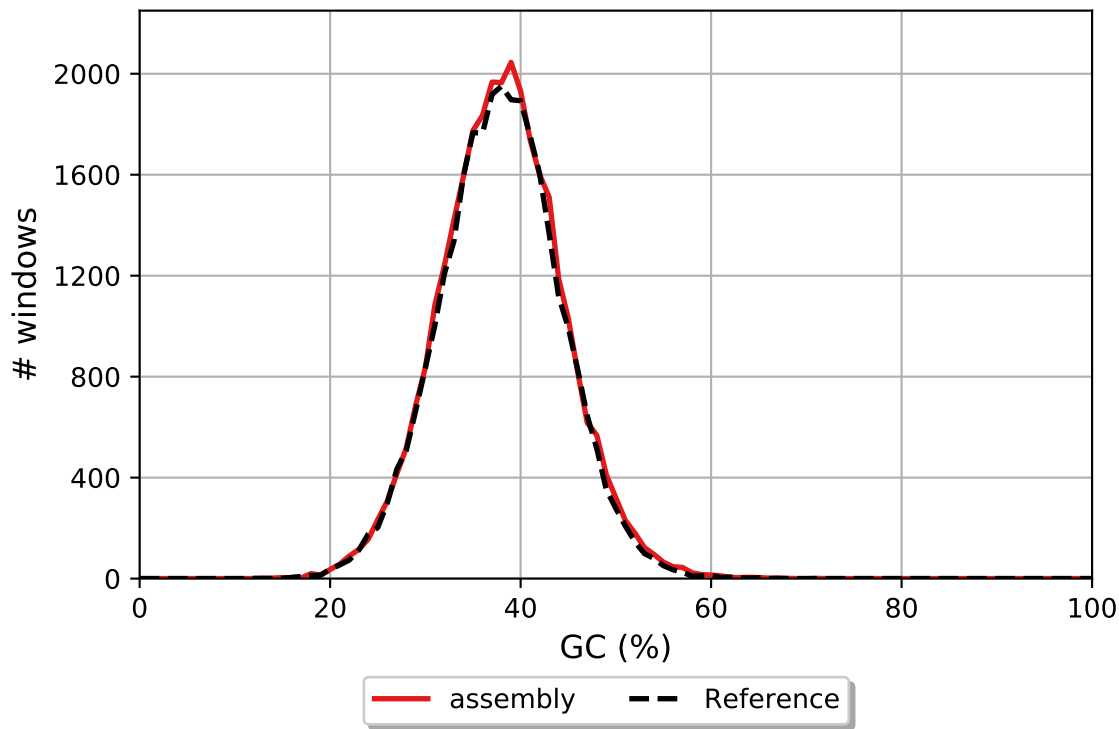


— assembly

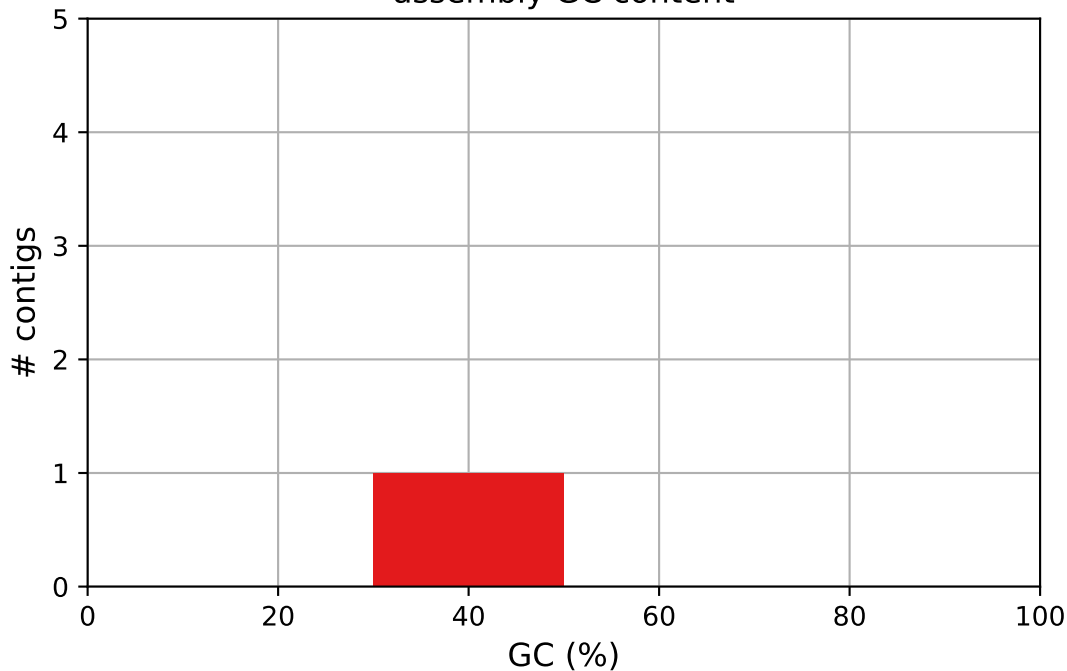
Cumulative length



## GC content



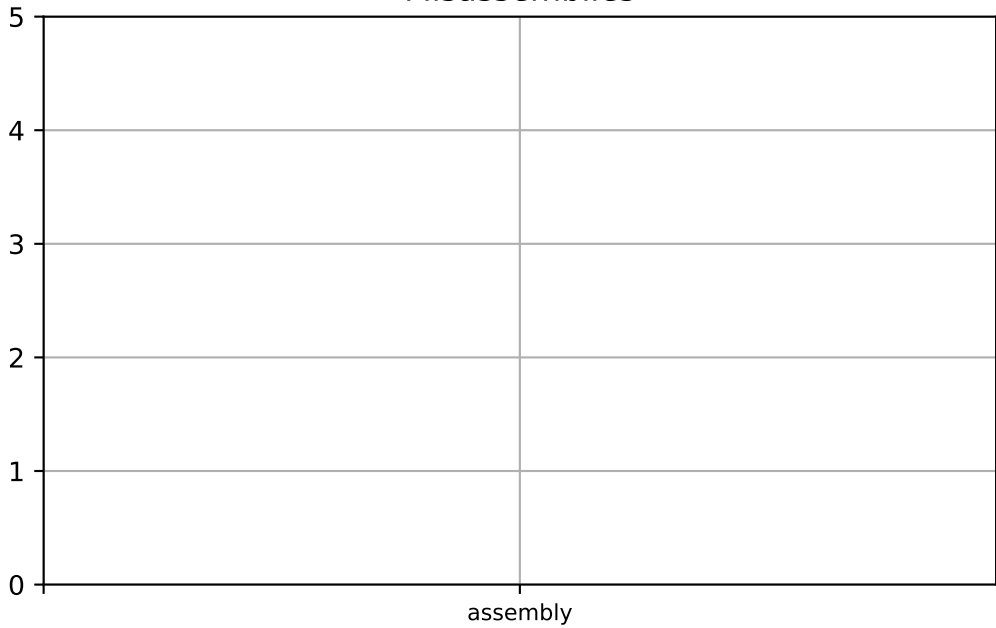
assembly GC content



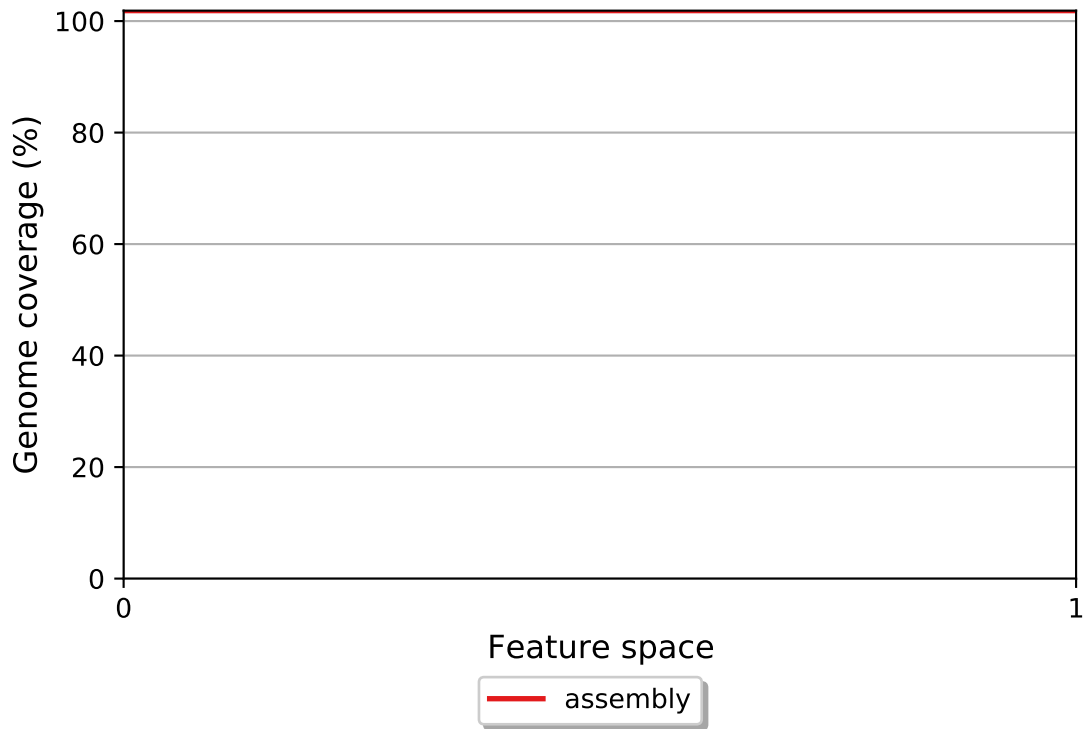
assembly



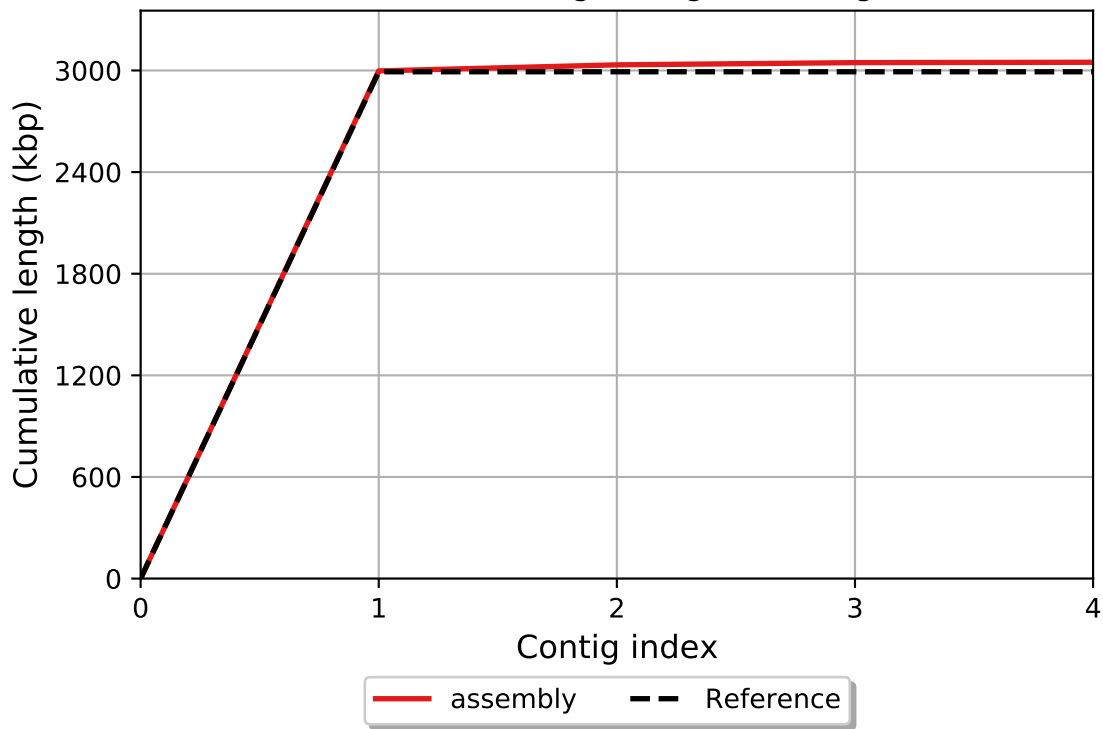
## Misassemblies



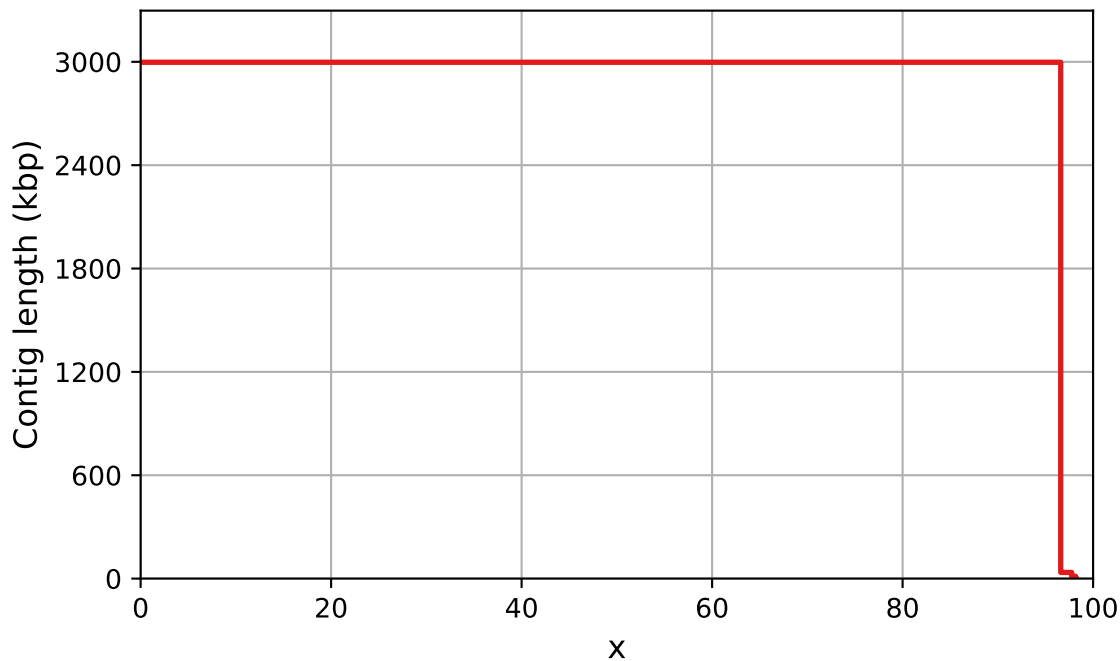
FRCurve (misassemblies)



Cumulative length (aligned contigs)

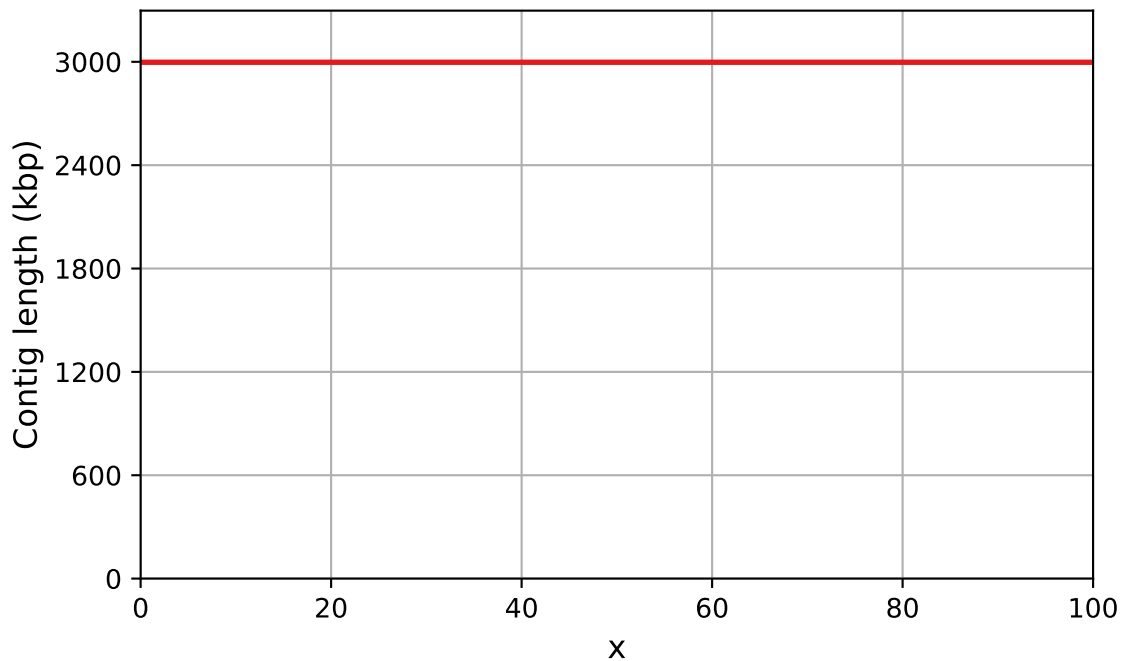


NAx



— assembly

## NGAx



— assembly